Abstract

A method for evaluating a sample for the presence or absence of multiple virus infections is disclosed. In one embodiment, this method comprises the step of evaluating a biological sample for nucleic acid sequences complementary to nucleotide primers and probes derived from the sequences of human parainfluenza virus 1, 2 and 3, respiratory syncytial virus A and B and influenza virus A and B. In another embodiment, the invention is an improved PCR method.